EXHIBIT 2

⧉ NCBI   **Blast 2 Sequences results**

| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: |1___| Mismatch: |-2___| gap open: |5___| gap extension: |2___|

x_dropoff: |50__| expect: |10.000| wordsize: |11__| Filter ☑ | Align |

| **Sequence 1** | gi 130_7635 | Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA | **Length** 2753 | (1 .. 2753) |
| **Sequence 2** | lcl|seq_2 | | **Length** 25 | (1 .. 25) |
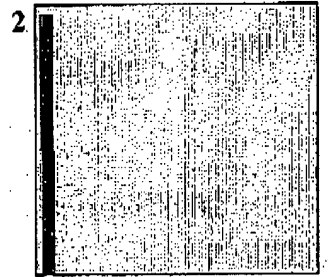
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 43.0 bits (22), Expect = 1.6
Identities = 24/25 (96%)
Strand = Plus / Minus
```

```
Query: 118  ctacacaaaaagcctggatcactca 142
             ||||||||||||||| |||||||||||
Sbjct: 25   ctacacaaaaagcttggatcactca 1
```

```
CPU time:      0.06 user secs.        0.05 sys. secs        0.11 total secs.

Lambda      K        H
  1.33     0.621     1.12

Gapped
Lambda      K        H
  1.33     0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
```

```
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
length of query: 2753
length of database: 5,006,917,935
effective HSP length: 25
effective length of query: 2728
effective length of database: 5,000,452,710
effective search space: 13641234992880
effective search space used: 13641234992880
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)
```